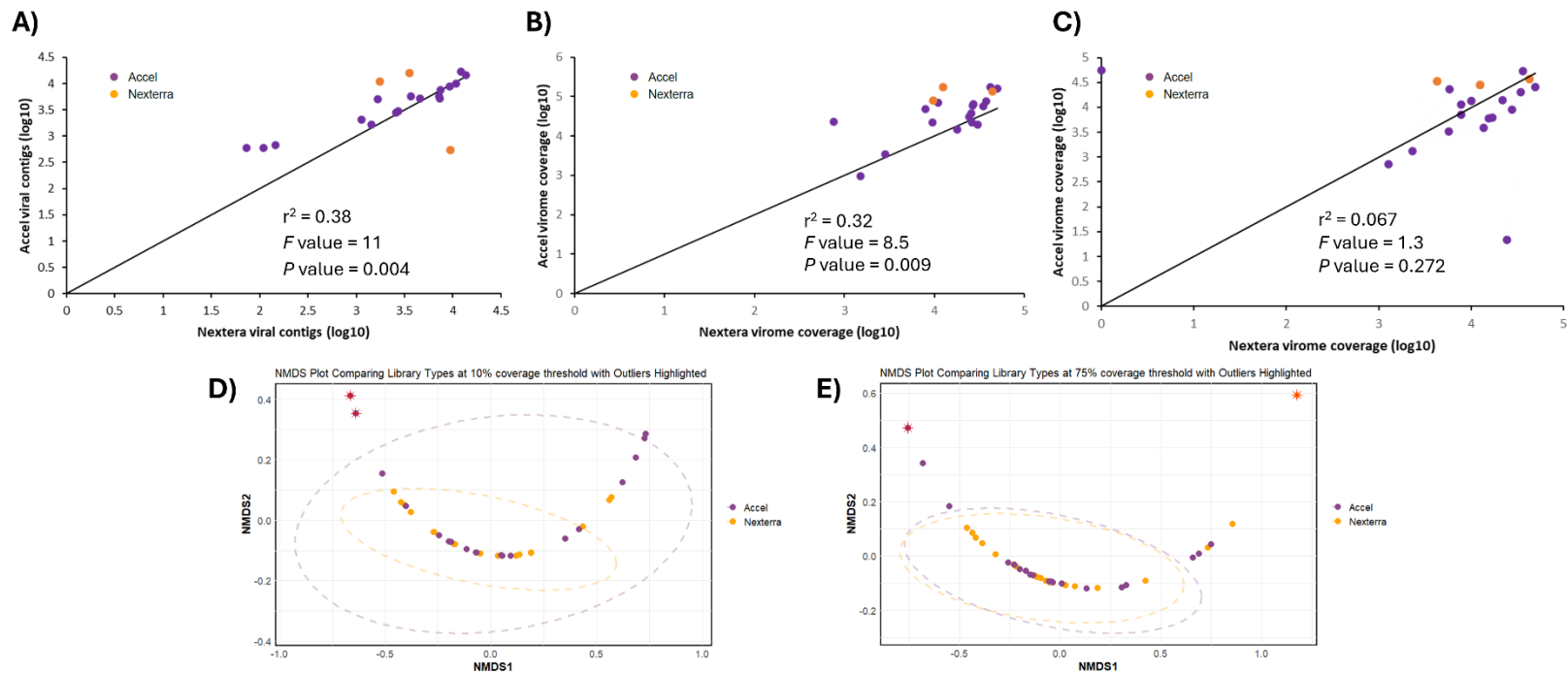
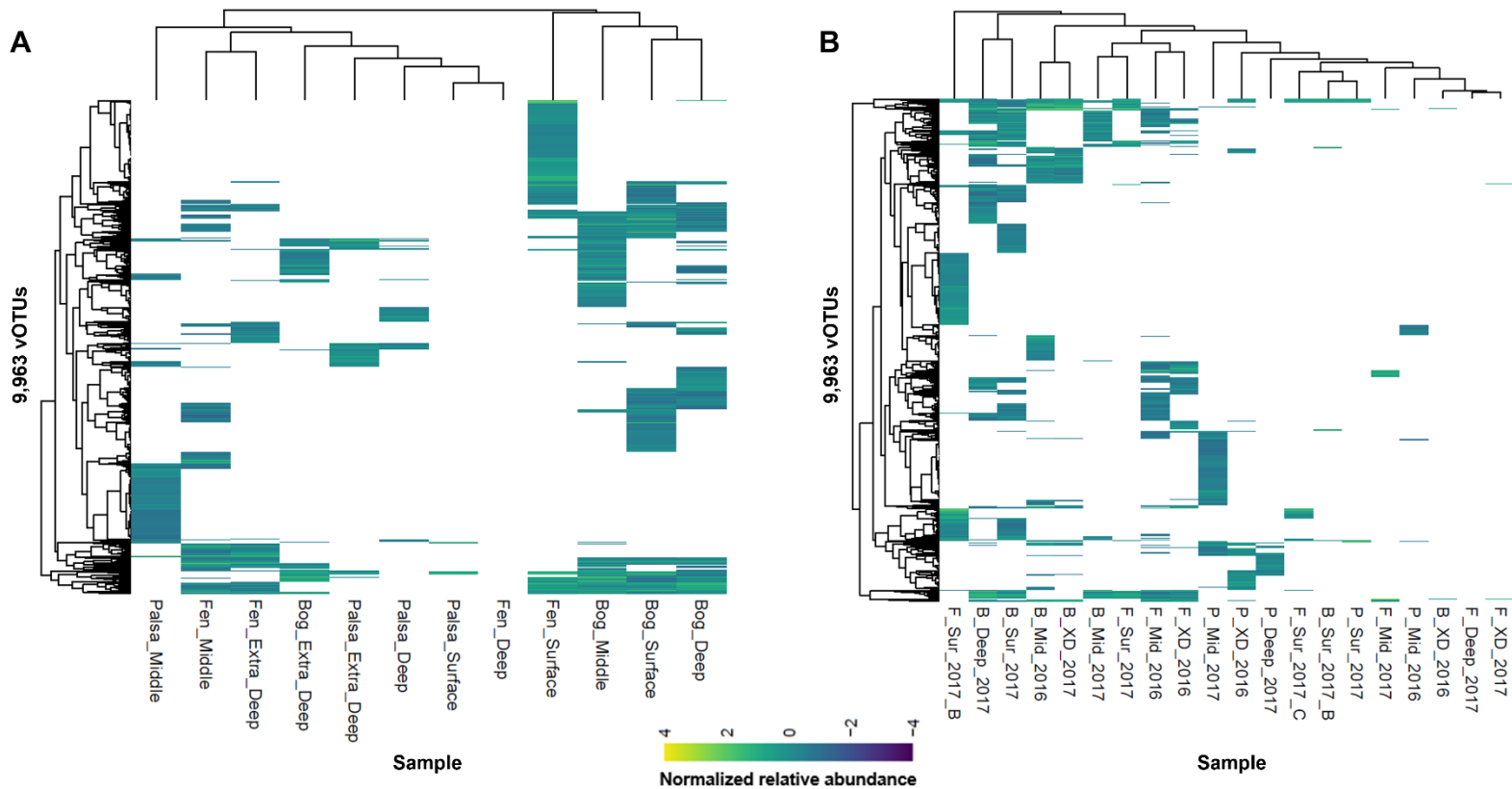




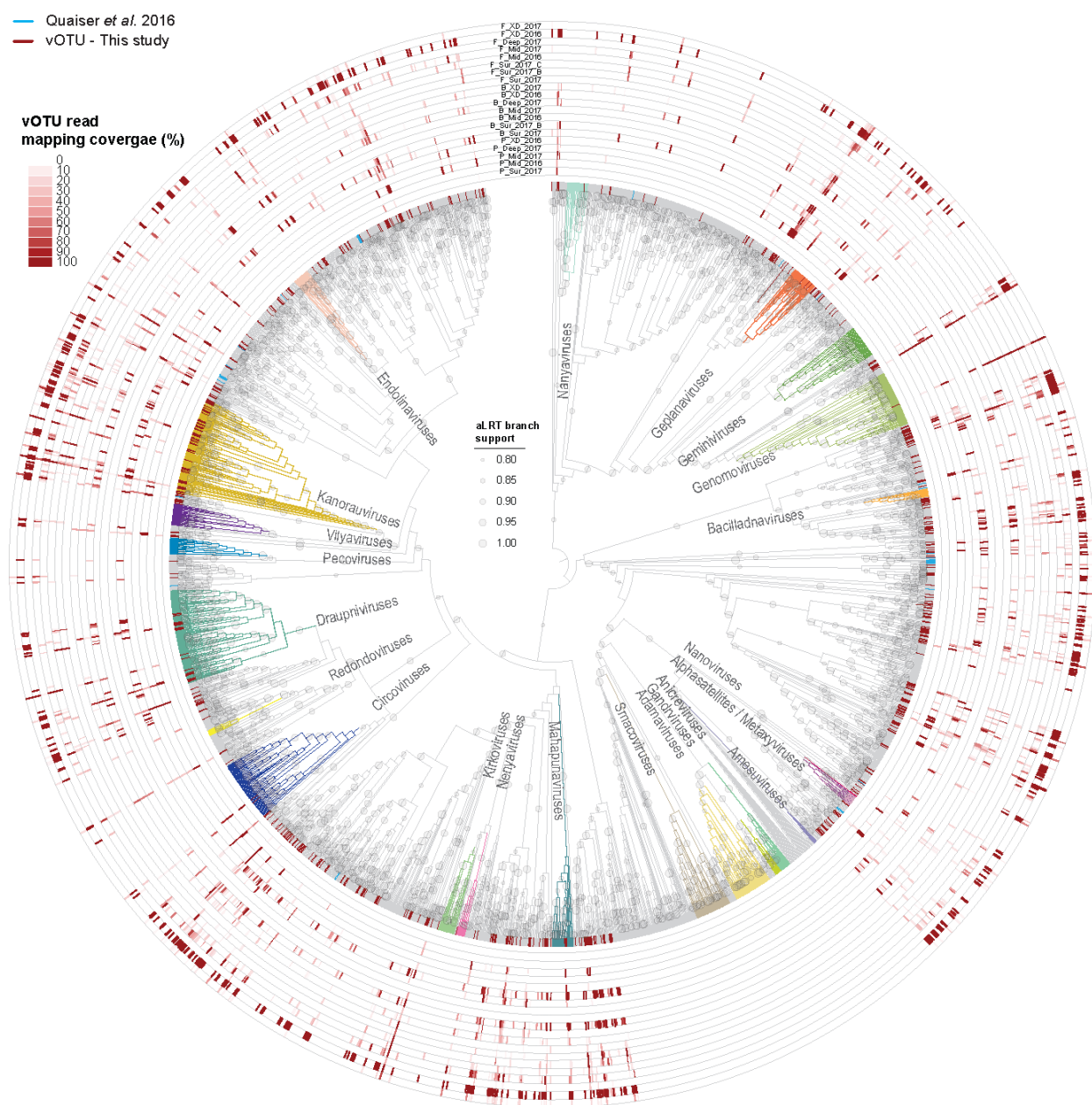
Supplementary Figure 1. Comparison of viral contig recovery and coverage between Nextera and Accel library preparation methods across 40 soil viromes. (A) Total number of viral contigs recovered per sample, showing consistent recovery across library methods. Read counts mapping to contigs detected by both kits at a relaxed (B) threshold and strict (C) threshold. NMDS plots of Bray-Curtis dissimilarities based on contig abundance, comparing library preparation methods at the relaxed (D) and strict (E) mapping thresholds. Samples cluster by individual rather than by library method, and PERMANOVA and ANOSIM tests indicate no significant differences between kits (PERMANOVA $p > 0.88$; ANOSIM $R < 0.02$, $p > 0.75$).



Supplementary Figure 2. vOTU diversity by depth and sample. (A) A heatmap comparing samples grouped by habitat and depth and (B) a heatmap of the 20 samples clustered using a Bray-Curtis dissimilarity metric based on vOTU normalized abundance.

Supplementary Figure 3. Phylogenetic comparison of ssDNA microvirus vOTUs to Les Pradeaux Mire.

Maximum likelihood phylogeny of MCP amino acid sequences encoded by the microvirus genomes available in GenBank, Les Pradeaux Mire⁷⁷, and vOTUs from this study. The phylogeny is represented as a cladogram and aLRT branch support >0.8 is shown. The MCP phylogenetic tree is rooted with sequences of bullaviruses represented with an orange clade and MCPs are shown in red nodes. The *sphagnum*-dominated peatland Les Pradeaux Mire microviruses (MCP)⁷⁷ are shown in blue. The percentage genome coverage of the mapped reads from each sample to the vOTUs is shown on the outside of the cladograms.



Supplementary Figure 4. Phylogenetic comparison of ssDNA cressdnavirus vOTUs to Les Pradeaux Mire.

Maximum likelihood phylogeny of Rep amino acid sequences encoded by cressdnaviruses available in GenBank, Les Pradeaux Mire⁷⁸, and vOTUs from this study. The phylogeny is represented as a cladogram and aLRT branch support >0.8 is shown. The Rep phylogenetic tree is midpoint rooted and classified cressdnavirus Reps in the phylogeny are shown with color coded clades whereas those from this study are shown in red nodes and representatives from the *sphagnum*-dominated peatland Les Pradeaux Mire (Rep)⁷⁸ are shown in blue. The percentage genome coverage of the mapped reads from each sample to the vOTUs is shown on the outside of the cladograms.